

BLASTP ALIGNMENT OF SEQ ID NO: 4 METALLOCARBOXYPEPTIDASE-LIKE POLYPEPTIDE WITH BOTHROPS JARARACA CARBOXYPEPTIDASE HOMOLOG SEQ ID NO: 20

Query: Metallo carboxypeptidase-like protein (SEQ ID 4)  
Subject: >gb|AAF01344.1| (AF190274) carboxypeptidase homolog [Bothrops jararaca] (SEQ ID NO: 20)  
Length = 416

Score = 826 (295.8 bits), Expect = 3.2e-82, P = 3.2e-82  
Identities = 152/.326 (46%), Positives = 219/326 (67%)

Query: 13 MIVPGGLGYDRSLAQHRQEIIVDKSVSPWSLET-YSYNIYHPMGEIYEWREISEKYKEW 71  
+L GL Y+ L + Q ++D+ + + Y+Y Y+ +I W +I+ + +V  
Sbjct: 82 ILQSGSLNVE-ILIDNLQAVLDRQLDNHARTAGYNEYKYSWEKIDAWTADIANENPSLV 140

Query: 72 TQHFGLGVTYETHPIYLYKISQPSGNPKIIMDCGIHAREWIAPAFCQWFVKEILQNHHKD 131  
++ +G T+E P+ LK+ +P N KK I++DCG HAREWI+PAFCQWFV+E ++ +  
Sbjct: 141 SRLQIGTTFEGRPMPLLKVGKPGVN-KKAIFIDCGFHAREWISPAFCQWFVREAVRTY GK 199

Query: 132 NSRIRKLLRNLDYFVLPVLNIDGYIYTWTTDLNRKSRSPHNNGTCTFGTDLNRNFNASWC 191  
+ + +LL LDFY+LPVLNIDGY+Y+W R+WRK+RS + TC GTD NRNF+A+WC  
Sbjct: 200 ETIMTQLLNKLDFYILPVLNIDGYVYSWKQSRMWRKTRSVNAGSTCIGTDPNRRNFDAAWC 259

Query: 192 SIGASRNCQDQTFCGTGPVSEPETKAVASFIESKKDDILCFLTMHSYGQLILTPYGYTKN 251  
S+GASRN +T+CG+ P SE ETKA+A FI + I +LT+HSY Q++L PY YT +  
Sbjct: 260 SVGASRNPCTSETYCGSKPESEKETKALADFIRNRRSIIQAYLTIHSYSQMLLYPYSYTYD 319

Query: 252 KSSNHPEMIQVGQKAANALKAKYGTNYRVGSSADILYASSGSSRDWARDIGIPFSYTFEL 311  
+SN+ ++ + ++A LK +GT Y G A +Y ++G S DWA D GI +++TFEL  
Sbjct: 320 LTSNNKKLNSIAKEAIRELKVLFGEITYGPGAATIPYAGGSDWAYDQGIKYAFTFEL 379

Query: 312 RDSGTYGFLPEAQIQPTCEETMEAV 337  
RD G YGF LPE+QI+PTCEETM AV  
Sbjct: 380 RDKGRYGFALPESQIKPTCEETMI AV 405

FIG: 1

# BLASTP ALIGNMENT OF SEQ ID NO: 4 METALLOCARBOXYPEPTIDASE-LIKE POLYPEPTIDE WITH HUMAN CARBOXYPEPTIDASE B MUTANT (G251N, D253R)-HCPB-(HIS)6-C-MYC SEQ ID NO: 21

Query: Carboxypeptidase-like protein (SEQ ID 4)  
 Subject: >sp|W13751|W13751 Carboxypeptidase B mutant (G251N,D253R)-HCPB-(His)6-c-myc (SEQ ID NO: 21)  
 Length = 349

Score = 811 (290.5 bits), Expect = 6.2e-81, P = 6.2e-81  
 Identities = 150/312 (48%), Positives = 206/312 (66%)

Query:	45	YSNYIYHPMGEIYEMRMREISEKYKEVVTQHFLGVTYETHPIYLYLKISQPSGNPKKIWM	104
Sbjct:		+SY Y+ I W ++++ + +++++ +G T+E IY LK+ + +G K I+MD	
	26	HSYEKYNKWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV GK-AGQNKPAIFMD	84
Query:	105	CGIHAREWIAPAFQWVFVKEILQNHKDNSRIRKLLRNLDYFVLPVLNIDGIYTWTDRL	164
Sbjct:		CG HAREWI+PAFCQWVF+E ++ + +LL LDYFVLPVLNIDGIYTWTDRL	
	85	CGFHAREWISPAFCQWVFVREAVRTYGREIQVTELLDKLDYFVLPVLNIDGIYTWTKSRF	144
Query:	165	WRKSRSPHNNGTCTGTDLNRNFNASWCISGASRNCQDQTFCTGTPVSEPETKAVASFIES	224
Sbjct:		WRK+RS H +C GTD NRNF+A WC IGASRN D+T+CG SE ETKA+A FI +	
	145	WRKTRSTHTGSSCIGTDPNRNFDAGWCEIGASRNPCEITYCGPAAESEKETKALADFIRN	204
Query:	225	KKDDILCFLTMHSYGQLILTPYGYTKNKNSSNHPEMIQVGQKAANALKAKYGTNYRVGSSA	284
Sbjct:		K I +LT+HSY Q+++ PY Y N+ E+ + + L + +GT Y G A	
	205	KLSSIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKELASLHGTYGPGA	264
Query:	285	DILYASSGSSRDWARDIGIPFSYTFELRDSGTGTYGFLPEAQIQPTCEETMEA---VLS-V	340
Sbjct:		+Y ++G+SRDWA D GI +S+TFELRD+G YGF+LPE+QI+ TCEET A V S V	
	265	TTIYPAAAGNSRDWAYDQIRYSFTFELRDTGRYGFLLPESQIRATCEETFLAIKYVASV	324
Query:	341	LDDVYAKHWHSD	352
Sbjct:		L+ +Y H H +	
	325	LEHLYHHHHHHE	336